



PCT10

ENTERED

## RAW SEQUENCE LISTING

DATE: 03/19/2003

PATENT APPLICATION: US/10/009,823A

TIME: 14:20:51

Input Set : A:\DAVIE150SEQLIST.TXT

Output Set: N:\CRF4\03192003\J009823A.raw

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4 <110> APPLICANT: Panaccio, Michael
5   Rosey, Everett Lee
6   Sinistaj, Meri
7   Hasse, Detlef
8   Parsons, Jim
9   Ankenbauer, Robert G.
11 <120> TITLE OF INVENTION: LAWSONIA DERIVED GENE AND RELATED FLGE
12   POLYPEPTIDES, PEPTIDES AND PROTEINS AND THEIR USES
15 <130> FILE REFERENCE: DAVI150.001APC
17 <140> CURRENT APPLICATION NUMBER: US 10/009,823A
C--> 18 <141> CURRENT FILING DATE: 2002-08-13
20 <150> PRIOR APPLICATION NUMBER: PCT/AU00/00437
21 <151> PRIOR FILING DATE: 2000-05-11
23 <150> PRIOR APPLICATION NUMBER: US 60/133,973
24 <151> PRIOR FILING DATE: 1999-05-13
26 <160> NUMBER OF SEQ ID NOS: 13
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 502
32 <212> TYPE: PRT
33 <213> ORGANISM: Lawsonia intracellularis
35 <400> SEQUENCE: 1
36 Met Met Gly Ser Leu Phe Ile Gly Ala Thr Gly Met Lys Thr His Ser
37 1 5 10 15
38 Thr Gly Leu Gly Thr Val Ser Asn Asn Ile Ala Asn Ala Asn Thr Ile
39 20 25 30
40 Gly Tyr Lys Gln Gln Gln Val Val Phe Gln Asp Leu Phe Ser Gln Asp
41 35 40 45
42 Leu Ala Ile Gly Ser Thr Gly Ser Gln Gly Pro Asn Gln Ala Gly Met
43 50 55 60
44 Gly Ala Gln Val Gly Ser Val Arg Thr Ile Phe Thr Gln Gly Ala Phe
45 65 70 75 80
46 Glu Pro Gly Asn Ser Val Thr Asp Leu Ala Ile Gly Gly Lys Gly Phe
47 85 90 95
48 Phe Gln Val Thr Leu Glu Asp Lys Val His Tyr Thr Arg Ala Gly Asn
49 100 105 110
50 Phe Arg Phe Thr Gln Asp Gly Phe Leu Asn Asp Pro Ser Gly Phe Thr
51 115 120 125
52 Leu Met Gly Ser Arg Ile Ser Asn Asn Pro Asn Ile Lys Lys Glu Thr
53 130 135 140
54 Leu Glu Pro Ile Gln Leu Asp Phe Asn Asp Pro Thr Val Ala Lys Ser
55 145 150 155 160
56 Pro Ala Lys Thr Ser Thr Ala Leu Asn Ala Val Val Asn Leu Gly Asp

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57                               165                               170                               175
58 Ser Thr Asp Lys Thr Gln Ser Glu Ala Asn Pro Tyr Phe Ala Leu Leu
59                               180                               185                               190
60 Glu Ser Trp Lys Gly Asn Gly Thr Pro Pro Ile Ser Thr Ser Asn Tyr
61                               195                               200                               205
62 Ser Tyr Ala Gln Pro Met Arg Val Tyr Asp Gln Gln Gly Asn Ser His
63                               210                               215                               220
64 Asp Ile Thr Val Tyr Phe Asp Gly Ala Pro Ser Ser Thr Gly Ser Lys
65 225                               230                               235                               240
66 Thr Phe Glu Tyr Leu Val Ala Met Asn Pro Ser Glu Asp Gly Ser Ala
67                               245                               250                               255
68 Ala Ser Gly Thr Asp Ser Ala Gly Leu Leu Met Ser Gly Thr Met Thr
69                               260                               265                               270
70 Phe Ser Ser Asn Gly Glu Leu Lys Asn Met Thr Ala Phe Thr Pro Thr
71                               275                               280                               285
72 Gly Ser Ala Thr Lys Asp Leu Asn Ala Trp Gln Pro Ala Pro Leu Val
73                               290                               295                               300
74 Asn Gly Leu Pro Gln Phe Ser Ala Asn Phe Val Gly Ala Gly Ile Gln
75 305                               310                               315                               320
76 Pro Leu Thr Leu Asp Phe Gly Ile Lys Ser Gln Gln Asn Met Trp Ala
77                               325                               330                               335
78 Gly Ala Pro Ala Ser Ala Ala Ala Ile Gly Thr Asp Ile Gly Lys Leu
79                               340                               345                               350
80 Pro Ser Met Met Pro Ile Gln Thr Ser Ser Gly Asn Ser Thr Ala Arg
81                               355                               360                               365
82 Asn Gly Ser Ser Ser Thr Arg Arg Tyr Ser Gln Asp Gly Tyr Pro Gln
83                               370                               375                               380
84 Gly Asp Leu Val Asp Val Thr Ile Thr Ser Glu Gly Lys Leu Gln Gly
85 385                               390                               395                               400
86 Lys Tyr Ser Asn Ser Gln Val Val Asp Phe Tyr Asn Ile Pro Leu Ala
87                               405                               410                               415
88 Arg Phe Thr Ser Glu Asp Gly Leu Arg Arg Glu Gly Asn Asn His Tyr
89                               420                               425                               430
90 Ser Ala Thr Leu Asp Ser Gly Gly Pro Glu Phe Gly Leu Pro Gly Thr
91                               435                               440                               445
92 Ser Asn Tyr Gly Lys Leu Ser Val Asn Gln Leu Glu Thr Ser Asn Val
93                               450                               455                               460
94 Asp Met Ser Arg Glu Met Val Asn Met Ile Ile Ile Gln Arg Gly Phe
95 465                               470                               475                               480
96 Gln Met Asn Ser Lys Ser Val Thr Thr Ala Asp Thr Met Leu Gln Lys
97                               485                               490                               495
98 Ala Leu Glu Leu Lys Arg
99                               500
102 <210> SEQ ID NO: 2
103 <211> LENGTH: 1509
104 <212> TYPE: DNA
105 <213> ORGANISM: Lawsonia intracellularis
107 <400> SEQUENCE: 2
108 atgatgggga gtttgtttat tgggtgaaca ggtatgaaaa cccatagtagt aggggttggtt 60

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109 actgtctcca ataatatgtc taacgcaa at accattgggt ataagcagca acaggtagtg 120
110 tttcaagacc tgtttagtca agatttagca ataggttcta ctggaagtca ggggccaaac 180
111 caggctggta tgggagcaca ggttggaagt gttcgacaca tttttacaca gggtgctttt 240
112 gaacctggca atagtgtaac agatcttgct attggtggaa aagggttttt tcaggttaca 300
113 ttagaggata aagtacacta tacacgagca ggggaattttc gttttactca agatggtttt 360
114 ttaaatgata ctacggtatt tactttaatg ggctcaagaa tatctaataa tcctaacata 420
115 aaaaaggaaa cccttgaacc aattcagtta gactttaatg atcctacagt agcaaagtct 480
116 cctgcaaaaa caagtacagc attaaacgct gtggtaaacc ttggtgatag tacagataaa 540
117 acacaaagtg aagctaatac atactttgca cttcttgaga gctggaaagg aaatggaaca 600
118 cctcctatct ctacatcaaa ctactcatat gcacaaccta tgagagtata tgatcaacaa 660
119 ggaaattctc acgatataac tgtatatctt gatggagcac cctcttcaac aggaagttaa 720
120 acatttgaat accttgtagc tatgaatcct agtgaagatg gaagtgtctg atcaggaaca 780
121 gatagtgcag gtctcttaac gtctggaact atgacatttt caagtaatgg cgaattaaaa 840
122 aatatgacag cttttactcc tactggctct gcaacaaaag atttaaattg atggcaacca 900
123 gcaccattag tcaatggttt accacagttt tcagcaaatt ttggtggtgc aggaatacac 960
124 cctttaacat tagacttttg aattaaaagc caacagaata tgtgggcagg agctccagca 1020
125 tccgctgctg ccataggtac agatattggg aaattgccat caatgatgcc aatacaaaac 1080
126 tccagcggta attctacagc aagaaatgga tcatcttcaa caagaagata tagccaagat 1140
127 ggttatctc agggagatct agtagatgtc acaattacct ctgaagggaa attacaaggt 1200
128 aagtatagta atagtcagggt tgttgatttt tataatatct ctttagcacg ctttacaagt 1260
129 gaggatggat taagacgaga agggaataac cattattccg caacacttga ctcagggtgg 1320
130 ccagagtttg gattgccagg aacatctaac tatggaaaac ttagtgtgaa tcaacttgag 1380
131 acttctaacy tagacatgag cagagaaatg gttaatatga ttattattca acgtggtttt 1440
132 cagatgaata gtaaatctgt tacaacagca gacacaatgc tacaaaaagc acttgaacta 1500
133 aagcgttaa 1509

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135 &lt;210&gt; SEQ ID NO: 3

136 &lt;211&gt; LENGTH: 21

137 &lt;212&gt; TYPE: DNA

138 &lt;213&gt; ORGANISM: Artificial Sequence

140 &lt;220&gt; FEATURE:

141 &lt;223&gt; OTHER INFORMATION: Oligonucleotide primer, RA170.

143 &lt;400&gt; SEQUENCE: 3

144 ctatttttag gagatgttat c

21

146 &lt;210&gt; SEQ ID NO: 4

147 &lt;211&gt; LENGTH: 22

148 &lt;212&gt; TYPE: DNA

149 &lt;213&gt; ORGANISM: Artificial Sequence

151 &lt;220&gt; FEATURE:

152 &lt;223&gt; OTHER INFORMATION: Oligonucleotide primer, RA171.

154 &lt;400&gt; SEQUENCE: 4

155 tacaaaatta acaataaaat ac

22

157 &lt;210&gt; SEQ ID NO: 5

158 &lt;211&gt; LENGTH: 38

159 &lt;212&gt; TYPE: DNA

160 &lt;213&gt; ORGANISM: Artificial Sequence

162 &lt;220&gt; FEATURE:

163 &lt;223&gt; OTHER INFORMATION: Oligonucleotide primer, FlaF.

W--&gt; 165 &lt;221&gt; NAME/KEY: misc\_feature

166 &lt;222&gt; LOCATION: (1)...(38)

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167 <223> OTHER INFORMATION: n = A,T,C or G
W--> 169 <400> 5
W--> 170 gcgaattcca tatgatgggg agtttggttta ttgntgcc 38
172 <210> SEQ ID NO: 6
173 <211> LENGTH: 40
174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Oligonucleotide primer, FlgE3'.
180 <400> SEQUENCE: 6
181 gctctagaga ctatgcatat taacgcttta gttcaagtgc 40
183 <210> SEQ ID NO: 7
184 <211> LENGTH: 477
185 <212> TYPE: PRT
186 <213> ORGANISM: Treponema phagedenis
188 <400> SEQUENCE: 7
189 Met Met Arg Ser Leu Phe Ser Gly Val Ser Gly Met Gln Asn His Gln
190 1 5 10 15
191 Gly Val Asn Pro Lys Glu Val Gly Leu Gly Val Met Val Ala Ser Gly
192 20 25 30
193 Val Asn Pro Lys Glu Val Gly Leu Gly Val Met Val Ala Ser Thr Arg
194 35 40 45
195 Met Asp Val Ile Gly Asn Asn Val Ala Asn Val Asn Thr Thr Gly Phe
196 50 55 60
197 Lys Arg Gly Arg Ile Asp Thr Val His Thr Gln Gly Ala Leu Gln Thr
198 65 70 75 80
199 Thr Gly Ile Asn Thr Asp Ile Ala Ile Val Asn Phe Gln Asp Leu Ile
200 85 90 95
201 Ser Gln Gln Leu Ser Gly Ala Ser Arg Pro Asn Glu Glu Val Gly Gln
202 100 105 110
203 Gly Asn Gly Phe Phe Ile Leu Lys Asp Gly Glu Lys Ser Phe Tyr Thr
204 115 120 125
205 Thr Ala Gly Ala Phe Gly Val Asp Arg Asp Gly Thr Leu Val Asn Pro
206 130 135 140
207 Ala Asn Gly Ala Cys Asn Leu Asp Lys Arg Leu Met Arg Val Gln Gly
208 145 150 155 160
209 Trp Met Ala Glu Asp Ile Glu Gly Gln Gln Ile Ile Asn Thr Ser Asp
210 165 170 175
211 Gln Pro Glu Leu Pro Glu Gly Ala Asn Gln Ala Asp Ile Leu Arg Ser
212 180 185 190
213 Thr Glu Asp Leu Ile Ile Pro Ile Gly Gln Lys Ile Asp Ala Lys Ala
214 195 200 205
215 Thr Thr Asp Val Ala Tyr Thr Trp Ala Thr Asp Phe Asn Val Tyr Asp
216 210 215 220
217 Thr Phe Gly Glu Gln His Lys Leu Gln Met Val Phe Ser Arg Val Pro
218 225 230 235 240
219 Gly Thr Asn Asn Gln Trp Leu Ala Thr Val Val Thr Asp Thr Ala Gly
220 245 250 255
221 Asn Val Thr Ala Pro Asn Val Asp Pro Glu Asn Gln Ala Gly Thr Glu

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```

222          260          265          270
223 Thr Arg Val Gly Ile Gly Thr Thr Asp Gly Ala Gly Gln Val Leu Val
224          275          280          285
225 Gln Ala Thr Glu Asn Thr Phe Ile Val Ser Phe Asp Asn Tyr Gly His
226          290          295          300
227 Leu Ala Ser Ser Tyr Asn Val Val Gly Ala Asn Pro Asp Glu Gly Gly
228 305          310          315          320
229 Ala Pro Thr Arg His Thr Phe Asn Ile Asn Asp Gln Ser Gly Ile Ile
230          325          330          335
231 Thr Gly Val Tyr Ser Asn Gly Ala Ser Leu Glu Gly Glu Ile Gly Thr
232          340          345          350
233 Ser Arg Asn Thr Ile Thr Gln Phe Ala Glu Arg Glu Ile Gly Gln Leu
234          355          360          365
235 Ala Leu Ala Gly Phe Ala Asn Gln Gly Gly Leu Glu Lys Ala Gly Glu
236          370          375          380
237 Ser Thr Thr Lys Ala Tyr Gln Gln Asp Gly Tyr Ala Met Gly Tyr Leu
238 385          390          395          400
239 Glu Asn Phe Lys Ile Thr Tyr Ile Gln Ser Asn Asn Ser Gly Ile Ala
240          405          410          415
241 Asn Ile Thr Val Ser Gly Val Met Gly Lys Gly Lys Leu Ile Ala Gly
242          420          425          430
243 Thr Leu Glu Met Ser Asn Val Asp Leu Thr Asp Gln Phe Thr Asp Met
244          435          440          445
245 Ile Ile Thr Gln Arg Gly Phe Gln Ala Gly Ala Lys Thr Ile Gln Thr
246          450          455          460
247 Ser Asp Thr Met Leu Glu Thr Val Leu Asn Leu Lys Arg
248 465          470          475
251 <210> SEQ ID NO: 8
252 <211> LENGTH: 462
253 <212> TYPE: PRT
254 <213> ORGANISM: Treponema pallidum
256 <400> SEQUENCE: 8
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258 1          5          10          15
259 Gly Val Asn Pro Lys Glu Val Gly Leu Gly Val Leu Ile Ala Ser Thr
260          20          25          30
261 Arg Met Asp Val Ile Gly Asn Asn Val Ala Asn Val Asn Thr Thr Gly
262          35          40          45
263 Phe Lys Arg Gly Arg Ile Asp Thr Val His Thr Gln Gly Ala Leu Gln
264          50          55          60
265 Thr Thr Gly Ile Asn Thr Asp Val Ser Ile Val Asn Phe Gln Asp Leu
266 65          70          75          80
267 Ile Ser Gln Gln Leu Ser Ala Ala Ala Arg Pro Asn Glu Glu Val Gly
268          85          90          95
269 Gln Gly Ser Gly Phe Phe Val Leu Lys Ser Gly Glu Lys Thr Phe Phe
270          100         105         110
271 Thr Arg Ala Gly Ala Phe Gly Val Asp Asn Ala Gly Thr Leu Val Asn
272          115         120         125
273 Pro Ala Asn Gly Ala Cys Asn Leu Asp Lys Arg Leu Met Arg Val Gln

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 34

Seq#:10; Xaa Pos. 197

VERIFICATION SUMMARY

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L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:165 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:169 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5  
L:170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0  
L:412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:192